RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/518,601

Source: PCT

Date Processed by STIC: 12-28-04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 4.2 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

> http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
<u>Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:</u>

1. EFS-Bio (<u><http://www.uspto.gov/ebc/efs/downloads/documents.htm></u>, EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04): U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/518,001

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics / Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ____ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino Numbering — The numbering under each 5ᵗʰ amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ____ Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length — Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing

6 ____ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) ____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ____ Skipped Sequences (OLD RULES) — Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence
(2) INFORMATION FOR SEQ ID NO X (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION SEQ ID NO X (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES" response to include the skipped sequences

8 ____ Skipped Sequences (NEW RULES) — Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents

10 ____ Invalid <213> Response — Per 1.823 of Sequence Rules, the only valid <213> responses are Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ✓ Use of <220> — Sequence(s) 2,4,6,8,10,12,14,16,18,20,22,24,26,35,36 missing the <220> Feature and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (See 1.823 of Sequence Rules)

12 ____ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n/Xaa — "n" can only represent a single nucleotide: "Xaa" can only represent a single amino acid

AMC - Biotechnology Systems Branch - 09/09/2003

PCT

```
RAW SEQUENCE LISTING                    DATE: 12/28/2004
PATENT APPLICATION:  US/10/518,001      TIME: 11:47:34

Input Set : D:\Protami1
Output Set: N:\CRF4\12282004\J518001.raw

   3 <110> APPLICANT: EBL GmbH
   5 <120> TITLE OF INVENTION: Method for the production of protamine
   7 <130> FILE REFERENCE: Protamin
C-->   9 <140> CURRENT APPLICATION NUMBER: US/10/518,001
C-->  10 <141> CURRENT FILING DATE: 2004-12-14
  12 <160> NUMBER OF SEQ ID NOS: 36
  14 <170> SOFTWARE: PatentIn Ver. 2.1
```

Does Not Comply
Corrected Diskette Needed

(PS. 1-5) ←

ERRORED SEQUENCES

pls insert <220> Feature,
whenever <221>, <222> or <223> is shown.

```
  42 <210> SEQ ID NO: 2
  43 <211> LENGTH: 33
  44 <212> TYPE: PRT
  45 <213> ORGANISM: Oncorhynchus mykiss
  46 <223> OTHER INFORMATION: aa sequence derived from ORF of nucleotide
  47       sequence
  49 <400> SEQUENCE: 2
  50 Met Pro Arg Arg Arg Arg Ser Ser Ser Arg Pro Val Arg Arg Arg Arg
  51  1               5                   10                  15
  53 Arg Pro Arg Val Ser Arg Arg Arg Arg Arg Arg Gly Gly Arg Arg Arg
  54              20                  25                  30
  56 Arg
  87 <210> SEQ ID NO: 4
  88 <211> LENGTH: 33
  89 <212> TYPE: PRT
  90 <213> ORGANISM: Oncorhynchus mykiss
  91 <223> OTHER INFORMATION: aa sequence derived from ORF of nucleotide
  92       sequence
  94 <400> SEQUENCE: 4
  95 Met Pro Arg Arg Arg Arg Ser Ser Arg Pro Pro Val Arg Arg Arg Arg
  96  1               5                   10                  15
  98 Arg Pro Arg Val Ser Arg Arg Arg Arg Arg Arg Gly Gly Arg Arg Arg
  99              20                  25                  30
 101 Arg
 132 <210> SEQ ID NO: 6
 133 <211> LENGTH: 33
 134 <212> TYPE: PRT
 135 <213> ORGANISM: Oncorhynchus mykiss
 136 <223> OTHER INFORMATION: aa sequence derived from ORF of nucleotide
 137       sequence
 139 <400> SEQUENCE: 6
 140 Met Pro Arg Arg Arg Arg Ser Ser Arg Arg Pro Val Arg Arg Arg Arg
```

pls insert <220>, whenever <221>, <222> or <223> is shown.

same error

See item #11 on error summary sheet.

```
            RAW SEQUENCE LISTING              DATE: 12/28/2004
            PATENT APPLICATION:  US/10/518,001    TIME: 11:47:34

            Input Set : D:\Protami1
            Output Set: N:\CRF4\12282004\J518001.raw
```
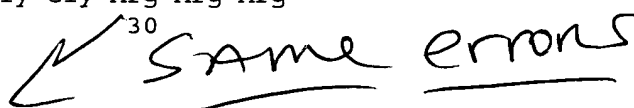
(acc)

← Same errors

```
141  1            5              10            15
143 Arg Pro Arg Val Ser Arg Arg Arg Arg Arg Arg Gly Gly Arg Arg Arg
144           20              25            30
146 Arg
177 <210> SEQ ID NO: 8
178 <211> LENGTH: 33
179 <212> TYPE: PRT
180 <213> ORGANISM: Oncorhynchus mykiss
181 <223> OTHER INFORMATION: aa sequence derived from ORF of nucleotide
182       sequence
184 <400> SEQUENCE: 8
185 Met Pro Arg Arg Arg Arg Ser Ser Ser Arg Pro Val Arg Arg Arg Arg
186  1            5              10            15
188 Arg Ala Arg Val Ser Arg Arg Arg Arg Arg Arg Gly Arg Arg Arg Arg
189           20              25            30
191 Arg
222 <210> SEQ ID NO: 10
223 <211> LENGTH: 33
224 <212> TYPE: PRT
225 <213> ORGANISM: Oncorhynchus mykiss
226 <223> OTHER INFORMATION: aa sequence derived from ORF of nucleotide
227       sequence
229 <400> SEQUENCE: 10
230 Met Pro Arg Arg Arg Arg Ser Ser Ser Arg Pro Val Arg Arg Arg Arg
231  1            5              10            15
233 Arg Pro Arg Val Ser Arg Arg Arg Arg Arg Arg Gly Arg Arg Arg Arg
234           20              25            30
236 Arg
267 <210> SEQ ID NO: 12
268 <211> LENGTH: 33
269 <212> TYPE: PRT
270 <213> ORGANISM: Oncorhynchus keta
271 <223> OTHER INFORMATION: aa sequence derived from ORF of nucleotide
272       sequence
274 <400> SEQUENCE: 12
275 Met Pro Arg Arg Arg Arg Ser Ser Ser Arg Pro Val Arg Arg Arg Arg
276  1            5              10            15
278 Arg Pro Arg Val Ser Arg Arg Arg Arg Arg Arg Gly Gly Arg Arg Arg
279           20              25            30
281 Arg
312 <210> SEQ ID NO: 14
313 <211> LENGTH: 33
314 <212> TYPE: PRT
315 <213> ORGANISM: Oncorhynchus mykiss
316 <223> OTHER INFORMATION: nucleotide sequence derived from amino acid
317       sequence
319 <400> SEQUENCE: 14
320 Met Pro Arg Arg Arg Arg Ser Ser Ser Arg Pro Val Arg Arg Arg Arg
321  1            5              10            15
```

RAW SEQUENCE LISTING   DATE: 12/28/2004
PATENT APPLICATION: US/10/518,001   TIME: 11:47:34

Input Set : **D:\Protami1**
Output Set: **N:\CRF4\12282004\J518001.raw**

```
323 Arg Ala Arg Val Ser Arg Arg Arg Arg Arg Arg Gly Gly Arg Arg Arg
324          20                25                30
326 Arg
354 <210> SEQ ID NO: 16
355 <211> LENGTH: 31
356 <212> TYPE: PRT
357 <213> ORGANISM: Oncorhynchus mykiss
358 <223> OTHER INFORMATION: nucleotide sequence derived from amino acid
359       sequence
361 <400> SEQUENCE: 16
362 Met Pro Arg Arg Arg Arg Ala Ser Arg Arg Val Arg Arg Arg Arg Arg
363   1           5                10                15
365 Pro Arg Val Ser Arg Arg Arg Arg Arg Gly Gly Arg Arg Arg Arg
366          20                25                30
393 <210> SEQ ID NO: 18
394 <211> LENGTH: 31
395 <212> TYPE: PRT
396 <213> ORGANISM: Oncorhynchus mykiss
397 <223> OTHER INFORMATION: nucleotide sequence derived from amino acid
398       sequence
400 <400> SEQUENCE: 18
401 Met Pro Arg Arg Arg Arg Ala Ser Arg Arg Ile Arg Arg Arg Arg Arg
402   1           5                10                15
404 Pro Arg Val Ser Arg Arg Arg Arg Arg Gly Gly Arg Arg Arg Arg
405          20                25                30
435 <210> SEQ ID NO: 20
436 <211> LENGTH: 33
437 <212> TYPE: PRT
438 <213> ORGANISM: Oncorhynchus mykiss
439 <223> OTHER INFORMATION: nucleotide sequence derived from amino acid
440       sequence
442 <400> SEQUENCE: 20
443 Met Pro Arg Arg Arg Arg Arg Ser Ser Ser Arg Pro Ile Arg Arg Arg
444   1           5                10                15
446 Arg Arg Pro Arg Val Ser Arg Arg Arg Arg Arg Gly Gly Arg Arg Arg
447          20                25                30
449 Arg
477 <210> SEQ ID NO: 22
478 <211> LENGTH: 31
479 <212> TYPE: PRT
480 <213> ORGANISM: Clupea harengus
481 <223> OTHER INFORMATION: nucleotide sequence derived from amino acid
482       sequence
484 <400> SEQUENCE: 22
485 Met Pro Arg Arg Arg Thr Arg Arg Ala Ser Arg Pro Val Arg Arg Arg
486   1           5                10                15
488 Arg Pro Arg Arg Val Ser Arg Arg Arg Arg Ala Arg Arg Arg Arg
489          20                25                30
518 <210> SEQ ID NO: 24
```

```
                RAW SEQUENCE LISTING              DATE: 12/28/2004
                PATENT APPLICATION:  US/10/518,001    TIME: 11:47:34

                Input Set : D:\Protami1
                Output Set: N:\CRF4\12282004\J518001.raw

    519 <211> LENGTH: 32
    520 <212> TYPE: PRT        Same erron
    521 <213> ORGANISM: Clupea harengus
    522 <223> OTHER INFORMATION: nucleotide sequence derived from amino acid
    523       sequence
    525 <400> SEQUENCE: 24
    526 Met Ala Arg Arg Arg Arg Ser Arg Arg Ala Ser Arg Pro Val Arg Arg
    527 1               5                   10                  15
    529 Arg Arg Pro Arg Arg Val Ser Arg Arg Arg Arg Ala Arg Arg Arg Arg
    530             20                  25                  30
    559 <210> SEQ ID NO: 26
    560 <211> LENGTH: 32
    561 <212> TYPE: PRT        Same erron
    562 <213> ORGANISM: Clupea harengus
    563 <223> OTHER INFORMATION: nucleotide sequence derived from amino acid
    564       sequence
    566 <400> SEQUENCE: 26
    567 Met Ala Arg Arg Arg Arg Ser Ser Ser Arg Pro Ile Arg Arg Arg Arg
    568 1               5                   10                  15
    570 Pro Arg Arg Arg Thr Thr Arg Arg Arg Arg Ala Gly Arg Arg Arg Arg
    571             20                  25                  30
    803 <210> SEQ ID NO: 35
    804 <211> LENGTH: 22
    805 <212> TYPE: PRT
    806 <213> ORGANISM: Artificial Sequence
W-->807 <220> FEATURE:
    807 <223> OTHER INFORMATION: Description of Artificial Sequence: cloning
    808       sequence for expression of Protamine
    810 <400> SEQUENCE: 35
    811 Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
    812 1               5                   10                  15
    813 Ala Gln Pro Ala Met Ala
    814             20
    817 <210> SEQ ID NO: 36
    818 <211> LENGTH: 33
    819 <212> TYPE: PRT
    820 <213> ORGANISM: Artificial Sequence
W-->821 <220> FEATURE:
    821 <223> OTHER INFORMATION: Description of Artificial Sequence: cloning
    822       sequence for expression of Protamine
    824 <400> SEQUENCE: 36
    825 Met Pro Arg Arg Arg Arg Ser Ser Ser Arg Pro Val Arg Arg Arg Arg
    826 1               5                   10                  15
    827 Arg Pro Arg Val Ser Arg Arg Arg Arg Arg Arg Gly Gly Arg Arg Arg
    828             20                  25                  30
    829 Arg
```

(handwritten annotations) pls insert this mandatory numeric identifier.

(handwritten) pls insert this mandatory numeric identifier.

(handwritten) see item #11 on error summary sheet

<210> 13
<211> 102
<212> DNA
<213> Oncorhynchus mykiss

<220>
<221> CDS
<222> (1)..(99)

<220>
<223> nucleotide sequence derived from amino acid
      sequence

<400> 13
atg ccc aga aga cgc aga tcc tcc agc cga cct gtc cgc agg cgc cgc   48
Met Pro Arg Arg Arg Arg Ser Ser Ser Arg Pro Val Arg Arg Arg Arg
 1   5   10   15

cgc gcn agg gtg tcc cga cgt cgt cgc agg aga gga ggc cgc agg agg   96
Arg Ala Arg Val Ser Arg Arg Arg Arg Arg Arg Gly Gly Arg Arg Arg
                20   25   30

cgt tag   102
Arg

pls explain "N" location.
See error explanation
on page 6.

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

VARIABLE LOCATION SUMMARY   DATE: 12/28/2004
PATENT APPLICATION: **US/10/518,001**   TIME: 11:47:35

Input Set : **D:\Protamil**
Output Set: **N:\CRF4\12282004\J518001.raw**

Use of n's or Xaa's(NEW RULES): *Error Explanation:* ✓
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
in <220> to <223> section, please explain location of n or Xaa, and which
residue n or Xaa represents.

Seq#:13; N Pos. 54
Seq#:15; N Pos. 21,30
Seq#:17; N Pos. 21,30
Seq#:21; N Pos. 27
Seq#:23; N Pos. 30
Seq#:27; N Pos. 30
Seq#:28; N Pos. 9,12,18,42,57,78,81,93,96
Seq#:33; Xaa Pos. 1,2,6,7,8,9,10,11,12,13,14,19,20,22,23,24,25,29,30,31,32
Seq#:33; Xaa Pos. 36

VERIFICATION SUMMARY   DATE: 12/28/2004
PATENT APPLICATION: **US/10/518,001**   TIME: 11:47:35

Input Set : **D:\Protami1**
Output Set: **N:\CRF4\12282004\J518001.raw**

L:9 M:270 C: Current Application Number differs, Replaced Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:49 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:2
L:94 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:4
L:139 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:6
L:184 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:8
L:229 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:10
L:274 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:12
L:304 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:48
L:319 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:14
L:345 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
L:361 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:16
L:384 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
L:400 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:18
L:442 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:20
L:468 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0
L:484 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:22
L:507 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:0
L:525 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:24
L:566 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:26
L:584 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:27
L:584 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:27
L:584 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:0
L:597 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:28
L:597 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:28
L:597 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:0
M:341 Repeated in SeqNo=28
L:729 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:33
L:729 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:33
L:729 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:0
M:341 Repeated in SeqNo=33
L:807 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:35
L:810 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:35
L:821 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:36
L:824 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:36